

SEQUENCE LISTING

<110> DREYFUS, MARC
LOPEZ, PASCAL

<120> MUTANT E. COLI STRAINS, AND THEIR USE FOR PRODUCING
RECOMBINANT POLYPEPTIDES

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<140> 09/762,481

<141> 2001-07-02

<150> PCT/FR99/01879

<151> 1999-07-29

<150> FR 98/10197

<151> 1998-08-07

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<170> PatentIn Ver. 2.1

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: CNRS
- (B) STREET: 3, rue Michel-Ange
- (C) CITY: PARIS
- (E) COUNTRY: FRANCE
- (F) POSTAL CODE: 75794 CEDEX 16

(ii) TITLE OF THE INVENTION: Mutant *E. coli* strains, and their use for producing recombinant polypeptides

(iii) NUMBER OF SEQUENCES: 6

(iv) COMPUTER-READABLE FORM:

- (A) TYPE OF MEDIUM: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(OEB)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) CONFIGURATION: linear

(ii) TYPE OF MOLECULE: DNA (genomic)

(ix) ADDITIONAL CHARACTERISTICS:

- (A) NAME: CDS
- (B) POSITION: 441..3623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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 758
 Lys Asp Val Leu Arg Glu Gly Gln Glu Val Ile Val Gln Ile Asp Lys
 95 100 105
 GAA GAG CGC GGC AAC AAA GGC GCG GCA TTA ACC ACC TTT ATC AGT CTG
 806
 Glu Glu Arg Gly Asn Lys Gly Ala Ala Leu Thr Thr Phe Ile Ser Leu
 110 115 120
 GCG GGT AGC TAT CTG GTT CTG ATG CCG AAC AAC CCG CGC GCG GGT GGC
 854
 Ala Gly Ser Tyr Leu Val Leu Met Pro Asn Asn Pro Arg Ala Gly Gly
 125 130 135
 ATT TCT CGC CGT ATC GAA GGC GAC GAC CGT ACC GAA TTA AAA GAA GCA
 902
 Ile Ser Arg Arg Ile Glu Gly Asp Asp Arg Thr Glu Leu Lys Glu Ala
 140 145 150
 CTG GCA AGC CTT GAA CTG CCG GAA GGC ATG GGG CTT ATC GTG CGC ACC
 950
 Leu Ala Ser Leu Glu Leu Pro Glu Gly Met Gly Leu Ile Val Arg Thr
 155 160 165 170
 GCT GGC GTC GGC AAA TCT GCT GAG GCG CTG CAA TGG GAT TTA AGC TTC
 998
 Ala Gly Val Gly Lys Ser Ala Glu Ala Leu Gln Trp Asp Leu Ser Phe
 175 180 185
 CGT CTG AAA CAC TGG GAA GCC ATC AAA AAA GCC GCT GAA AGC CGC CCG
 1046
 Arg Leu Lys His Trp Glu Ala Ile Lys Lys Ala Ala Glu Ser Arg Pro
 190 195 200
 GCC CCG TTC CTG ATT CAT CAG GAG AGC AAC GTA ATC GTT CGC GCA TTC
 1094
 Ala Pro Phe Leu Ile His Gln Glu Ser Asn Val Ile Val Arg Ala Phe

205	210	215
CGC GAT TAC TTA CGT CAG GAC ATC GGC GAA ATC CTT ATC GAT AAC CCG 1142		
Arg Asp Tyr Leu Arg Gln Asp Ile Gly Glu Ile Leu Ile Asp Asn Pro 220 225 230		
AAA GTG CTC GAA CTG GCA CGT CAG CAT ATC GCT GCA TTA GGT CGC CCG 1190		
Lys Val Leu Glu Leu Ala Arg Gln His Ile Ala Ala Leu Gly Arg Pro 235 240 245 250		
GAT TTC AGC AGC AAA ATC AAA CTG TAC ACC GGC GAG ATC CCG CTG TTC 1238		
Asp Phe Ser Ser Lys Ile Lys Leu Tyr Thr Gly Glu Ile Pro Leu Phe 255 260 265		
AGC CAC TAC CAG ATC GAG TCA CAG ATC GAG TCC GCC TTC CAG CGT GAA 1286		
Ser His Tyr Gln Ile Glu Ser Gln Ile Glu Ser Ala Phe Gln Arg Glu 270 275 280		
GTT CGT CTG CCG TCT GGT GGT TCC ATT GTT ATC GAC AGC ACC GAA GCG 1334		
Val Arg Leu Pro Ser Gly Gly Ser Ile Val Ile Asp Ser Thr Glu Ala 285 290 295		
TTA ACG GCC ATC GAC ATC AAC TCC GCA CGC GCG ACC CGC GGC GGC GAT 1382		
Leu Thr Ala Ile Asp Ile Asn Ser Ala Arg Ala Thr Arg Gly Gly Asp 300 305 310		
ATC GAA GAA ACC GCG TTT AAC ACT AAC CTC GAA GCT GCC GAT GAG ATT 1430		
Ile Glu Glu Thr Ala Phe Asn Thr Asn Leu Glu Ala Ala Asp Glu Ile 315 320 325 330		
GCT CGT CAG CTG CGC CTG CGT GAC CTC GGC GGC CTG ATT GTT ATC GAC 1478		
Ala Arg Gln Leu Arg Leu Arg Asp Leu Gly Gly Leu Ile Val Ile Asp 335 340 345		

TTC ATC GAC ATG ACG CCA GTA CGC CAC CAG CGT GCG GTA GAA AAC CGT
1526

Phe Ile Asp Met Thr Pro Val Arg His Gln Arg Ala Val Glu Asn Arg
350 355 360

CTG CGT GAA GCG GTG CGT CAG GAC CGT GCG CGT ATT CAA ATC AGC CAT
1574

Leu Arg Glu Ala Val Arg Gln Asp Arg Ala Arg Ile Gln Ile Ser His
365 370 375

ATT TCT CGC TTT GGC CTG CTG GAA ATG TCC CGT CAG CGC CTG AGC CCA
1622

Ile Ser Arg Phe Gly Leu Leu Glu Met Ser Arg Gln Arg Leu Ser Pro
380 385 390

TCA CTG GGT GAA TCC AGT CAT CAC GTT TGT CCG CGT TGT TCT GGT ACT
1670

Ser Leu Gly Glu Ser Ser His His Val Cys Pro Arg Cys Ser Gly Thr
395 400 405 410

GGC ACC GTG CGT GAC AAC GAA TCG CTG TCG CTC TCT ATT CTG CGT CTG
1718

Gly Thr Val Arg Asp Asn Glu Ser Leu Ser Leu Ser Ile Leu Arg Leu
415 420 425

ATC GAA GAA GAA GCG CTG AAA GAG AAC ACC CAG GAA GTT CAC GCC ATT
1766

Ile Glu Glu Glu Ala Leu Lys Glu Asn Thr Gln Glu Val His Ala Ile
430 435 440

GTT CCT GTG CCA ATC GCT TCT TAC CTG CTG AAT GAA AAA CGT TCT GCG
1814

Val Pro Val Pro Ile Ala Ser Tyr Leu Leu Asn Glu Lys Arg Ser Ala
445 450 455

GTA AAT GCC ATT GAA ACT CGT CAG GAC GGT GTG CGC TGT GTA ATT GTG
1862

Val Asn Ala Ile Glu Thr Arg Gln Asp Gly Val Arg Cys Val Ile Val
460 465 470

CCA AAC GAT CAG ATG GAA ACC CCG CAC TAC CAC GTG CTG CGC GTG CGT
 1910
 Pro Asn Asp Gln Met Glu Thr Pro His Tyr His Val Leu Arg Val Arg
 475 480 485 490

AAA GGG GAA GAA ACC CCA ACC TTA AGC TAC ATG CTG CCG AAG CTG CAT
 1958
 Lys Gly Glu Glu Thr Pro Thr Leu Ser Tyr Met Leu Pro Lys Leu His
 495 500 505

GAA GAA GCG ATG GCG CTG CCG TCT GAA GAA GAG TTC GCT GAA CGT AAG
 2006
 Glu Glu Ala Met Ala Leu Pro Ser Glu Glu Glu Phe Ala Glu Arg Lys
 510 515 520

CGT CCG GAA CAA CCT GCG CTG GCA ACC TTT GCC ATG CCG GAT GTG CCG
 2054
 Arg Pro Glu Gln Pro Ala Leu Ala Thr Phe Ala Met Pro Asp Val Pro
 525 530 535

CCT GCG CCA ACG CCA GCT GAA CCT GCC GCG CCT GTT GTA GCT CCA GCA
 2102
 Pro Ala Pro Thr Pro Ala Glu Pro Ala Ala Pro Val Val Ala Pro Ala
 540 545 550

CCG AAA GCT GCA CCG GCA ACA CCA GCA GCT CCT GCA CAA CCT GGG CTG
 2150
 Pro Lys Ala Ala Pro Ala Thr Pro Ala Ala Pro Ala Gln Pro Gly Leu
 555 560 565 570

TTG AGC CGC TTC TTC GGC GCA CTG AAA GCG CTG TTC AGC GGT GGT GAA
 2198
 Leu Ser Arg Phe Phe Gly Ala Leu Lys Ala Leu Phe Ser Gly Gly Glu
 575 580 585

GAA ACC AAA CCG ACC GAG CAA CCA GCA CCG AAA GCA GAA GCG AAA CCG
 2246
 Glu Thr Lys Pro Thr Glu Gln Pro Ala Pro Lys Ala Glu Ala Lys Pro
 590 595 600

GAA CGT CAA CAG GAT CGT CGC AAG CCT CGT CAG AAC AAC CGC CGT GAC
 2294
 Glu Arg Gln Gln Asp Arg Arg Lys Pro Arg Gln Asn Asn Arg Arg Asp

605	610	615
CGT AAT GAG CGC CGC GAC ACC CGT AGT GAA CGT ACT GAA GGC AGC GAT 2342		
Arg Asn Glu Arg Arg Asp Thr Arg Ser Glu Arg Thr Glu Gly Ser Asp 620 625 630		
AAT CGC GAA GAA AAC CGT CGT AAT CGT CGC CAG GCA CAG CAG CAG ACT 2390		
Asn Arg Glu Glu Asn Arg Arg Asn Arg Arg Gln Ala Gln Gln Gln Thr 635 640 645 650		
GCC GAG ACG CGT GAG AGC CGT CAG CAG GCT GAG GTA ACG GAA AAA GCG 2438		
Ala Glu Thr Arg Glu Ser Arg Gln Gln Ala Glu Val Thr Glu Lys Ala 655 660 665		
CGT ACC GCC GAC GAG CAG CAA GCG CCG CGT CGT GAA CGT AGC CGC CGC 2486		
Arg Thr Ala Asp Glu Gln Gln Ala Pro Arg Arg Glu Arg Ser Arg Arg 670 675 680		
CGT AAT GAT GAT AAA CGT CAG GCG CAA CAA GAA GCG AAG GCG CTG AAT 2534		
Arg Asn Asp Asp Lys Arg Gln Ala Gln Gln Glu Ala Lys Ala Leu Asn 685 690 695		
GTT GAA GAG CAA TCT GTT CAG GAA ACC GAA CAG GAA GAA CGT GTA CGT 2582		
Val Glu Glu Gln Ser Val Gln Glu Thr Glu Gln Glu Glu Arg Val Arg 700 705 710		
CCG GTT CAG CCG CGT CGT AAA CAG CGT CAG CTC AAT CAG AAA GTG CGT 2630		
Pro Val Gln Pro Arg Arg Lys Gln Arg Gln Leu Asn Gln Lys Val Arg 715 720 725 730		
TAC GAG CAA AGC GTA GCC GAA GAA GCG GTA GTC GCA CCG GTG GTT GAA 2678		
Tyr Glu Gln Ser Val Ala Glu Glu Ala Val Val Ala Pro Val Val Glu 735 740 745		

GAA ACT GTC GCT GCC GAA CCA ATT GTT CAG GAA GCG CCA GCT CCA CGC
 2726
 Glu Thr Val Ala Ala Glu Pro Ile Val Gln Glu Ala Pro Ala Pro Arg
 750 755 760

ACA GAA CTG GTG AAA GTC CCG CTG CCA GTC GTA GCG CAA ACT GCA CCA
 2774
 Thr Glu Leu Val Lys Val Pro Leu Pro Val Val Ala Gln Thr Ala Pro
 765 770 775

GAA CAG CAA GAA GAG AAC AAT GCT GAT AAC CGT GAC AAC GGT GGC ATG
 2822
 Glu Gln Gln Glu Glu Asn Asn Ala Asp Asn Arg Asp Asn Gly Gly Met
 780 785 790

CCG CGT CGT TCT CGC CGC TCG CCT CGT CAC CTG CGC GTA AGT GGT CAG
 2870
 Pro Arg Arg Ser Arg Arg Ser Pro Arg His Leu Arg Val Ser Gly Gln
 795 800 805 810

CGT CGT CGT CGC TAT CGT GAC GAG CGT TAT CCA ACC CAG TCG CCA ATG
 2918
 Arg Arg Arg Arg Tyr Arg Asp Glu Arg Tyr Pro Thr Gln Ser Pro Met
 815 820 825

CCG TTG ACC GTA GCG TGC GCG TCT CCG GAA CTG GCC TCT GGC AAA GTC
 2966
 Pro Leu Thr Val Ala Cys Ala Ser Pro Glu Leu Ala Ser Gly Lys Val
 830 835 840

TGG ATC CGC TAT CCA ATT GTA CGT CCG CAA GAT GTA CAG GTT GAA GAG
 3014
 Trp Ile Arg Tyr Pro Ile Val Arg Pro Gln Asp Val Gln Val Glu Glu
 845 850 855

CAG CGC GAA CAG GAA GAA GTA CAT GTG CAG CCG ATG GTG ACT GAG GTC
 3062
 Gln Arg Glu Gln Glu Glu Val His Val Gln Pro Met Val Thr Glu Val
 860 865 870

CCT GTC GCC GCC GCT ATC GAA CCG GTT GTT AGC GCG CCA GTT GTT GAA
 3110

Pro Val Ala Ala Ala Ile Glu Pro Val Val Ser Ala Pro Val Val Glu
 875 880 885 890
 GAA GTG GCC GGT GTC GTA GAA GCC CCC GTT CAG GTT GCC GAA CCG CAA
 3158
 Glu Val Ala Gly Val Val Glu Ala Pro Val Gln Val Ala Glu Pro Gln
 895 900 905
 CCG GAA GTG GTT GAA ACG ACG CAT CCT GAA GTG ATC GCT GCC GCG GTA
 3206
 Pro Glu Val Val Glu Thr Thr His Pro Glu Val Ile Ala Ala Ala Val
 910 915 920
 ACT GAA CAG CCG CAG GTG ATT ACC GAG TCT GAT GTT GCC GTA GCC CAG
 3254
 Thr Glu Gln Pro Gln Val Ile Thr Glu Ser Asp Val Ala Val Ala Gln
 925 930 935
 GAA GTT GCA GAA CAA GCA GAA CCG GTG GTT GAA CCG CAG GAA GAG ACG
 3302
 Glu Val Ala Glu Gln Ala Glu Pro Val Val Glu Pro Gln Glu Glu Thr
 940 945 950
 GCA GAT ATT GAA GAA GTT GTC GAA ACT GCT GAG GTT GTA GTT GCT GAA
 3350
 Ala Asp Ile Glu Glu Val Val Glu Thr Ala Glu Val Val Val Ala Glu
 955 960 965 970
 CCT GAA GTT GTT GCT CAA CCT GCC GCG CCA GTA GTC GCT GAA GTC GCA
 3398
 Pro Glu Val Val Ala Gln Pro Ala Ala Pro Val Val Ala Glu Val Ala
 975 980 985
 GCA GAA GTT GAA ACG GTA GCT GCG GTC GAA CCT GAG GTC ACC GTT GAG
 3446
 Ala Glu Val Glu Thr Val Ala Ala Val Glu Pro Glu Val Thr Val Glu
 990 995 1000
 CAT AAC CAC GCT ACC GCG CCA ATG ACG CGC GCT CCA GCA CCG GAA TAT
 3494
 His Asn His Ala Thr Ala Pro Met Thr Arg Ala Pro Ala Pro Glu Tyr

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      1005              1010              1015
GTT CCG GAG GCA CCG CGT CAC AGT GAC TGG CAG CGC CCT ACT TTT GCC
3542
Val Pro Glu Ala Pro Arg His Ser Asp Trp Gln Arg Pro Thr Phe Ala
1020              1025              1030

TTC GAA GGT AAA GGT GCC GCA GGT GGT CAT ACG GCA ACA CAT CAT GCC
3590
Phe Glu Gly Lys Gly Ala Ala Gly Gly His Thr Ala Thr His His Ala
1035              1040              1045              1050

TCT GCC GCT CCT GCG CGT CCG CAA CCT GTT GAG TAATAATTAG CTCAAAGTAA
3643
Ser Ala Ala Pro Ala Arg Pro Gln Pro Val Glu

      1055              1060

TCAAGCCCTG GTAAGTGC
3661

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 amino acids
- (B) TYPE: amino acid
- (D) CONFIGURATION: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

Met Lys Arg Met Leu Ile Asn Ala Thr Gln Gln Glu Glu Leu Arg Val
 1              5              10              15

Ala Leu Val Asp Gly Gln Arg Leu Tyr Asp Leu Asp Ile Glu Ser Pro
      20              25              30

Gly His Glu Gln Lys Lys Ala Asn Ile Tyr Lys Gly Lys Ile Thr Arg
      35              40              45

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Ile Glu Pro Ser Leu Glu Ala Ala Phe Val Asp Tyr Gly Ala Glu Arg
 50 55 60
 His Gly Phe Leu Pro Leu Lys Glu Ile Ala Arg Glu Tyr Phe Pro Ala
 65 70 75 80
 Asn Tyr Ser Ala His Gly Arg Pro Asn Ile Lys Asp Val Leu Arg Glu
 85 90 95
 Gly Gln Glu Val Ile Val Gln Ile Asp Lys Glu Glu Arg Gly Asn Lys
 100 105 110
 Gly Ala Ala Leu Thr Thr Phe Ile Ser Leu Ala Gly Ser Tyr Leu Val
 115 120 125
 Leu Met Pro Asn Asn Pro Arg Ala Gly Gly Ile Ser Arg Arg Ile Glu
 130 135 140
 Gly Asp Asp Arg Thr Glu Leu Lys Glu Ala Leu Ala Ser Leu Glu Leu
 145 150 155 160
 Pro Glu Gly Met Gly Leu Ile Val Arg Thr Ala Gly Val Gly Lys Ser
 165 170 175
 Ala Glu Ala Leu Gln Trp Asp Leu Ser Phe Arg Leu Lys His Trp Glu
 180 185 190
 Ala Ile Lys Lys Ala Ala Glu Ser Arg Pro Ala Pro Phe Leu Ile His
 195 200 205
 Gln Glu Ser Asn Val Ile Val Arg Ala Phe Arg Asp Tyr Leu Arg Gln
 210 215 220
 Asp Ile Gly Glu Ile Leu Ile Asp Asn Pro Lys Val Leu Glu Leu Ala
 225 230 235 240
 Arg Gln His Ile Ala Ala Leu Gly Arg Pro Asp Phe Ser Ser Lys Ile
 245 250 255
 Lys Leu Tyr Thr Gly Glu Ile Pro Leu Phe Ser His Tyr Gln Ile Glu
 260 265 270

Ser Gln Ile Glu Ser Ala Phe Gln Arg Glu Val Arg Leu Pro Ser Gly
 275 280 285
 Gly Ser Ile Val Ile Asp Ser Thr Glu Ala Leu Thr Ala Ile Asp Ile
 290 295 300
 Asn Ser Ala Arg Ala Thr Arg Gly Gly Asp Ile Glu Glu Thr Ala Phe
 305 310 315 320
 Asn Thr Asn Leu Glu Ala Ala Asp Glu Ile Ala Arg Gln Leu Arg Leu
 325 330 335
 Arg Asp Leu Gly Gly Leu Ile Val Ile Asp Phe Ile Asp Met Thr Pro
 340 345 350
 Val Arg His Gln Arg Ala Val Glu Asn Arg Leu Arg Glu Ala Val Arg
 355 360 365
 Gln Asp Arg Ala Arg Ile Gln Ile Ser His Ile Ser Arg Phe Gly Leu
 370 375 380
 Leu Glu Met Ser Arg Gln Arg Leu Ser Pro Ser Leu Gly Glu Ser Ser
 385 390 395 400
 His His Val Cys Pro Arg Cys Ser Gly Thr Gly Thr Val Arg Asp Asn
 405 410 415
 Glu Ser Leu Ser Leu Ser Ile Leu Arg Leu Ile Glu Glu Glu Ala Leu
 420 425 430
 Lys Glu Asn Thr Gln Glu Val His Ala Ile Val Pro Val Pro Ile Ala
 435 440 445
 Ser Tyr Leu Leu Asn Glu Lys Arg Ser Ala Val Asn Ala Ile Glu Thr
 450 455 460
 Arg Gln Asp Gly Val Arg Cys Val Ile Val Pro Asn Asp Gln Met Glu
 465 470 475 480
 Thr Pro His Tyr His Val Leu Arg Val Arg Lys Gly Glu Glu Thr Pro
 485 490 495
 Thr Leu Ser Tyr Met Leu Pro Lys Leu His Glu Glu Ala Met Ala Leu

500					505					510					
Pro	Ser	Glu	Glu	Glu	Phe	Ala	Glu	Arg	Lys	Arg	Pro	Glu	Gln	Pro	Ala
		515					520					525			
Leu	Ala	Thr	Phe	Ala	Met	Pro	Asp	Val	Pro	Pro	Ala	Pro	Thr	Pro	Ala
		530					535					540			
Glu	Pro	Ala	Ala	Pro	Val	Val	Ala	Pro	Ala	Pro	Lys	Ala	Ala	Pro	Ala
		545					550					555			
Thr	Pro	Ala	Ala	Pro	Ala	Gln	Pro	Gly	Leu	Leu	Ser	Arg	Phe	Phe	Gly
Ala	Leu	Lys	Ala	Leu	Phe	Ser	Gly	Gly	Glu	Glu	Thr	Lys	Pro	Thr	Glu
Gln	Pro	Ala	Pro	Lys	Ala	Glu	Ala	Lys	Pro	Glu	Arg	Gln	Gln	Asp	Arg
Arg	Lys	Pro	Arg	Gln	Asn	Asn	Arg	Arg	Asp	Arg	Asn	Glu	Arg	Arg	Asp
Thr	Arg	Ser	Glu	Arg	Thr	Glu	Gly	Ser	Asp	Asn	Arg	Glu	Glu	Asn	Arg
Arg	Asn	Arg	Arg	Gln	Ala	Gln	Gln	Gln	Thr	Ala	Glu	Thr	Arg	Glu	Ser
Arg	Gln	Gln	Ala	Glu	Val	Thr	Glu	Lys	Ala	Arg	Thr	Ala	Asp	Glu	Gln
Gln	Ala	Pro	Arg	Arg	Glu	Arg	Ser	Arg	Arg	Arg	Asn	Asp	Asp	Lys	Arg
Gln	Ala	Gln	Gln	Glu	Ala	Lys	Ala	Leu	Asn	Val	Glu	Glu	Gln	Ser	Val
Gln	Glu	Thr	Glu	Gln	Glu	Glu	Arg	Val	Arg	Pro	Val	Gln	Pro	Arg	Arg
Lys	Gln	Arg	Gln	Leu	Asn	Gln	Lys	Val	Arg	Tyr	Glu	Gln	Ser	Val	Ala

Glu	Glu	Ala	Val	Val	Ala	Pro	Val	Val	Glu	Glu	Thr	Val	Ala	Ala	Glu	
			740					745					750			
Pro	Ile	Val	Gln	Glu	Ala	Pro	Ala	Pro	Arg	Thr	Glu	Leu	Val	Lys	Val	
		755					760					765				
Pro	Leu	Pro	Val	Val	Ala	Gln	Thr	Ala	Pro	Glu	Gln	Gln	Glu	Glu	Asn	
	770					775					780					
Asn	Ala	Asp	Asn	Arg	Asp	Asn	Gly	Gly	Met	Pro	Arg	Arg	Ser	Arg	Arg	
785					790					795					800	
Ser	Pro	Arg	His	Leu	Arg	Val	Ser	Gly	Gln	Arg	Arg	Arg	Arg	Tyr	Arg	
			805					810						815		
Asp	Glu	Arg	Tyr	Pro	Thr	Gln	Ser	Pro	Met	Pro	Leu	Thr	Val	Ala	Cys	
			820					825					830			
Ala	Ser	Pro	Glu	Leu	Ala	Ser	Gly	Lys	Val	Trp	Ile	Arg	Tyr	Pro	Ile	
		835					840					845				
Val	Arg	Pro	Gln	Asp	Val	Gln	Val	Glu	Glu	Gln	Arg	Glu	Gln	Glu	Glu	
	850					855					860					
Val	His	Val	Gln	Pro	Met	Val	Thr	Glu	Val	Pro	Val	Ala	Ala	Ala	Ile	
865					870					875					880	
Glu	Pro	Val	Val	Ser	Ala	Pro	Val	Val	Glu	Glu	Val	Ala	Gly	Val	Val	
				885					890					895		
Glu	Ala	Pro	Val	Gln	Val	Ala	Glu	Pro	Gln	Pro	Glu	Val	Val	Glu	Thr	
			900					905					910			
Thr	His	Pro	Glu	Val	Ile	Ala	Ala	Ala	Val	Thr	Glu	Gln	Pro	Gln	Val	
		915					920					925				
Ile	Thr	Glu	Ser	Asp	Val	Ala	Val	Ala	Gln	Glu	Val	Ala	Glu	Gln	Ala	
	930					935					940					
Glu	Pro	Val	Val	Glu	Pro	Gln	Glu	Glu	Thr	Ala	Asp	Ile	Glu	Glu	Val	
945					950					955					960	

Val Glu Thr Ala Glu Val Val Val Ala Glu Pro Glu Val Val Ala Gln
 965 970 975
 Pro Ala Ala Pro Val Val Ala Glu Val Ala Ala Glu Val Glu Thr Val
 980 985 990
 Ala Ala Val Glu Pro Glu Val Thr Val Glu His Asn His Ala Thr Ala
 995 1000 1005
 Pro Met Thr Arg Ala Pro Ala Pro Glu Tyr Val Pro Glu Ala Pro Arg
 1010 1015 1020
 His Ser Asp Trp Gln Arg Pro Thr Phe Ala Phe Glu Gly Lys Gly Ala
 1025 1030 1035 1040
 Ala Gly Gly His Thr Ala Thr His His Ala Ser Ala Ala Pro Ala Arg
 1045 1050 1055
 Pro Gln Pro Val Glu
 1060

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) CONFIGURATION: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGGCTGCAGT TTCCGTGTCC ATCCTTG
 27

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) CONFIGURATION: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGGAGATCTT GATTACTTTG AGCTAA
26

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) CONFIGURATION: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTGCAGATAG CCCGCCTAAT GAGCGGGCTT TTTTTTCTGC AG
42

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) CONFIGURATION: linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

10 GCGGTGGTTA AGAAACCAAA C
21